

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 2, 2002, 00:24:09 : Search time 4358.45 Seconds

(without alignments)
11318.063 Million cell updates/sec

Title: US-09-856-979-6

Perfect score: 1695

Sequence: 1 ccgcgcattcttcgtgtga.....tccatcaagccgcgcgaatg 1695

Scoring table: IDENTITY_MDC

Gapop 10.0 , Gapept 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: gb_ba:*
2: gb_hg:*
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26: em_ro:*
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29: em_vl:*
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31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
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35: em_hcg_rod:*
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37: em_hcg_vrt:*
38: em_sy:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1695	100.0	1695	6 BD013095	BD013095 Method fo
2	1695	100.0	1695	23 BD010123	BD010123 Method fo
3	1695	100.0	2275	6 BD013093	BD013093 Method fo
4	1695	100.0	2275	23 BD010121	BD010121 Method fo
5	1695	100.0	5349	6 A71437	A71437 Sequence 7
6	1695	100.0	5349	6 AR207455	AR207455 Sequence
7	1695	100.0	6539	6 E31991	E31991 Mutated bar
8	1695	100.0	6548	6 A60109	A60109 Sequence 2
9	1695	100.0	6548	6 A76916	A76916 Sequence 2
10	1695	100.0	6548	6 AR098308	AR098308 Sequence
11	1695	100.0	6548	6 E31990	E31990 Mutated bar
12	1695	100.0	7492	6 BD013094	BD013094 Method fo
13	1695	100.0	7492	23 BD010122	BD010122 Method fo
14	1693.4	99.9	2407	6 A23333	A23333 E1 gene, TA
15	1693.4	99.9	2407	6 AR007519	AR007519 Sequence
16	1693.4	99.9	2407	6 AR084085	AR084085 Sequence
17	1693.4	99.9	2407	6 I47736	I47736 Sequence 8
18	1693.4	99.9	170226	6 AP003450	AP003450 Oryza sat
19	1690.4	99.7	6667	6 AX118825	AX118825 Sequence
20	1687	99.5	1687	6 AX118836	AX118836 Sequence
21	365	21.5	365	6 BD013096	BD013096 Method fo
22	365	21.5	365	23 BD010124	BD010124 Method fo
23	365	21.5	5228	6 BD013092	BD013092 Method fo
24	365	21.5	5228	23 BD010120	BD010120 Method fo
25	234	13.8	141942	2 AC130725	AC130725 Oryza sat
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28	85	5.0	146670	8 AP003250	AP003250 Oryza sat
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ALIGNMENTS

RESULT 1
BD013095 1695 bp DNA linear PAT 02-AUG-2002
LOCUS BD013095
DEFINITION Method for producing male-sterile plant.
ACCESSION BD013095
VERSION BD013095.1 GI:22093284
KEYWORDS WO 0124616-A/6.
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartioideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS Hamada,K. and Nakakido,F.
TITLE Method for producing male-sterile plant

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: WO 0124616-A 6 12-APR-2001;
JAPAN TOBACCO INC, KAZUYUKI HAMADA, FUMIO NAKAKIDO
COMMENT OS Oryza sativa (rice)
PN WO 0124616-A/6
PD 12-APR-2001
PF 12-SEP-2000 WO 2000JP006222
PR 30-SEP-1999 JP 99P 279307
PI KAZUYUKI HAMADA, FUMIO NAKAKIDO
PC A01H5/00, C12N15/11, C12N15/63, C12N15/82
CC E1 promoter
FH Key Location/Qualifiers.
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/db_xref="taxon:4530"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
BD010123
ID BD010123 standard. DNA; PLN: 1695 BP.
XX BD010123;
XX
SV BD010123.1

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XX 08-FEB-2002 (Rel. 70, Created)
DT 08-FEB-2002 (Rel. 70, Last updated, Version 1)
XX Method for producing male-sterile plant.
DE JP 03075934-T/6.
XX
XX Oryza sativa
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae;
OC Oryzaeae; Oryza.
XX
XX [1]
RN 1-1695
RA Hamada K., Nakakido F.;
RT "Method for producing male-sterile plant";
RL Patent number JP03075934-T/6, 16-MAR-2001.
XX JAPAN TOBACCO INC, KAZUYUKI HAMADA, FUMIO NAKAKIDO.
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XX OS Oryza sativa (rice)
CC PN JP 03075934-T/6
CC PD 16-MAR-2001
CC PF 12-SEP-2000 JP 200006222
CC PR 30-SEP-1999 JP 99P 279307
CC PI KAZUYUKI HAMADA, FUMIO NAKAKIDO
CC PC A01H5/00, C12N15/11, C12N15/63, C12N15/82
CC CC
CC FH Key Location/Qualifiers
CC FT 1. 1695
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	996	CAAGAAGCGAAGAAGCAAAAGTTTAAAGCTGTGTCAAAAAAATATAGCTAGAGCGCTTCCAGAT <td>937</td>	937
QY	1321	ATGCTTCTATCTCAGCGCAGACCAATAGGGGCAAAATTTACTATATTTTGGCATATTAAAC <td>1380</td>	1380
Db	936	ATGCTTCTATCTCAGCGCAGACCAATAGGGGCAAAATTTACTATATTTTGGCATATTAAAC <td>877</td>	877
QY	1381	CACGTAAAGAGCTCTACACCTCAACCTTACCTGTTGAACAGCGTCTTTCGTGGCCAAAGGTAG <td>1440</td>	1440
Db	876	CACGTAAAGAGCTCTACACCTTCAACCTTGTGAACAGCGTCTTTCGTGGCCAAAGGTAG <td>817</td>	817
QY	1441	AATGCACCTAATGAGCGGAGCAACGCTTTCACCGTGTACTGCTATCATCTGTAGAC <td>1500</td>	1500
Db	816	AATGCACCTAATGAGCGGAGCAACGCTTTCACCGTGTACTGCTATCATCTGTAGAC <td>757</td>	757
QY	1501	GGTGAAGCGGTGAGCGTCTTTCGCAATACCGTCTGTGTGTGGAGCACTTGGCCAC <td>1560</td>	1560
Db	756	GGTGAAGCGGTGAGCGTCTTTCGCAATACCGTCTGTGTGTGGAGCACTTGGCCAC <td>697</td>	697
QY	1561	GGTTCACCGGTGATGACGTGCGCAATATTCGCGCGGTGTGGCGGCGCTTACAAAAAGCA <td>1620</td>	1620
Db	696	GGTTCACCGGTGATGACGTGCGCAATATTCGCGCGGTGTGGCGGCGCTTACAAAAAGCA <td>637</td>	637
QY	1621	CACACGCAACCGCGGCCACGATTAACCATTCCTAGCATTCGCGGTGTCCAGCAGAGATCCAT <td>1680</td>	1680
Db	636	CACACGCAACCGCGGCCACGATTAACCATTCCTAGCATTCGCGGTGTCCAGCAGAGATCCAT <td>577</td>	577
QY	1681	CAAGCGCTGCGCATG 1695 <td></td>	
Db	576	CAAGCGCTGCGCATG 562 <td></td>	
RESULT 5			
A71437		5349 bp	DNA
LOCUS	A71437		Linear
DEFINITION	Sequence 7 from Patent WO9810081.		PAT 07-MAY-1998
ACCESSION	A71437		
VERSION	A71437.1		GI:4775050
KEYWORDS			
SOURCE	unidentified.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 5349)		
AUTHORS	Michielsen, F. and Williams, M.		
TITLE	IMPROVED BARSTAR GENE		
JOURNAL	Patent: WO 9810081-A 7 12-MAR-1998;		
	MICHELIS, FRANK (BE)		
FEATURES	Location/Qualifiers		
SOURCE	1..5349		
	/organism="unidentified"		
	/db_xref="taxon:32644"		
BASE COUNT	1339 a 1253 c 1290 g 1487 t		
ORIGIN			
Query Match	100.0%; Score 1695; DB 6; Length 5349;		
Best Local Similarity	100.0%; P-Id: 0;		
Matches 1695; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	CCGAGATCCCTTGTGTGATGATGTTTATTTAAATTAATATTATTCGAAATACCTACC	60
Db	2278	CCGAGATCCCTTGTGTGATGATGTTTATTTAAATTAATATTATTCGAAATACCTACC	2337
QY	61	ATATATAGTAGACTTGTCAACGTGCAAGACTTCCATATCCGCGCAATACCATACAGACA	120

Db	2338	AAATATATGATGACTGCAACCTGCAGAAAGCTCCAACTGCGCGACATACCAATATGAGAA	2397
OY	121	TCCAAACCACTTAATATCATATTAACAAACATCGATTTGTTAGTCAGACATATATTTAGAGTGG	180
Db	2398	TCCAAACCACTTAATATCATATTAACAAACATCGATTTGTTAGTCAGACATATATTTAGAGTGG	2457
OY	181	AACAAACATATACCAATTAACATATATGAGAGTATATTTGGCTAACTCTCAATTCATATATCT	240
Db	2458	AACAAACATATACCAATTAACATATATGAGAGTATATTTGGCTAACTCTCAATTCATATATCT	2517
OY	241	GATGAGTATATCTGCTCAATTTATAGCGCTCCAGAAACAAATATTCATATCTTGGACAAAT	300
Db	2518	GATGAGTATATCTGCTCAATTTATAGCGCTCCAGAAACAAATATTCATATCTTGGACAAAT	2577
OY	301	GTGGAGCATGGAGCTGTGTCATATTTTTCATATCTCTATTAACAGTGGAAAGAGTATGAT	360
Db	2578	GTGGAGCATGGAGCTGTGTCATATTTTTCATATCTCTATTAACAGTGGAAAGAGTATGAT	2637
OY	361	TATATATGACAGAGAAACATCTCTGAGATCCCTTCCACATGAGCATATGTCGTAAGAACAG	420
Db	2638	TATATATGACAGAGAAACATCTCTGAGATCCCTTCCACATGAGCATATGTCGTAAGAACAG	2697
OY	421	ATACAGCTGTACGTATGTTGTATATGACAGCTCAATGCCATTTTCTCGAAGCATGTTCCAG	480
Db	2698	ATACAGCTGTACGTATGTTGTATATGACAGAGCTCAATGCCATTTTCTCGAAGCATGTTCCAG	2737
OY	481	ACATGATGATTTCTCGGATCCTTGGAGGAGCCCTGAAATTTGGAACACATTAGTTAGTT	540
Db	2758	ACATGATGATTTCTCGGATCCTTGGAGGAGCCCTGAAATTTGGAACACATTAGTTAGTT	2817
OY	541	TTATGATCAATATGCTTGCGTTATATCTACTGATGAATGGCATTTTCTGTAACTGAGTTTTC	600
Db	2818	TTATGATCAATATGCTTGCGTTATATCTACTGATGAATGGCATTTTCTGTAACTGAGTTTTC	2877
OY	601	TACCATCTCCACAGAGAAATTAAGCTAATACCTGTCCCAAGAGTGGTCCGCAATTTTGACCAA	660
Db	2878	TACCATCTCCACAGAGAAATTAAGCTAATACCTGTCCCAAGAGTGGTCCGCAATTTTGACCAA	2937
OY	661	ATGAAAGATACACAGACGATTTGCAAGAAATGCGCAATCTGCGAAAGAGCGGAAATTAATGTAT	720
Db	2938	ATGAAAGATACACAGACGATTTGCAAGAAATGCGCAATCTGCGAAAGAGCGGAAATTAATGTAT	2997
OY	721	TCTACATACATGCAAGCAGAACATATGATATGTTGGCCACACAGAGACCCCGCAGATATAG	780
Db	2998	TCTACATACATGCAAGCAGAACATATGATATGTTGGCCACACAGAGACCCCGCAGATATAG	3057
OY	781	TTCCCTGTTCTTCCACAGCAGAAATTTCCGCAACATGATATAGTCTCCCAACATGAATATCCAA	840
Db	3058	TTCCCTGTTCTTCCACAGCAGAAATTTCCGCAACATGATATAGTCTCCCAACATGAATATCCAA	3117
OY	841	ACCACATCGGCTCAGAGAAAGTATGATTAAGAAAGGCACTAATTTGATATTTTCTCTACA	900
Db	3118	ACCACATCGGCTCAGAGAAAGTATGATTAAGAAAGGCACTAATTTGATATTTTCTCTACA	3177
OY	901	AAGCAATATATTAATAGCAACTTGACATCCGCAACCAACAGCTTTGGATGATGACTTTGGCG	960
Db	3178	AAGCAATATATTAATAGCAACTTGACATCCGCAACCAACAGCTTTGGATGATGACTTTGGCG	3237
OY	961	CATGAATATGGCAATCTGACATCTTGCTCACTGTGCAATCTCTCCGAAATATGAGAGGCA	1020
Db	3238	CATGAATATGGCAATCTGACATCTTGCTCACTGTGCAATCTCTCCGAAATATGAGAGGCA	3297
OY	1021	TAGCTTCGTGTGTGTGTGTGTGGGATATTAACGCTGCTTAACACTTTTGTGTTCTGATCG	1080
Db	3298	TAGCTTCGTGTGTGTGTGTGTGGGATATTAACGCTGCTTAACACTTTTGTGTTCTGATCG	3357
OY	1081	ATCTGTGTTAAGAGCACTGCTGTTTATTAACCACTTAACAAATGCTACTATTAATCTCTCAAG	1140
Db	3358	ATCTGTGTTAAGAGCACTGCTGTTTATTAACCACTTAACAAATGCTACTATTAATCTCTCAAG	3417
OY	1141	ACCCTATATCGCCAAAGAAAGATACCTTGGCGCTGGGAGATTGAGACCGTTGAAGAGGAAC	1200
Db	3418	ACCCTATATCGCCAAAGAAAGATACCTTGGCGCTGGGAGATTGAGACCGTTGAAGAGGAAC	3477

QY 1201 AACGAATACAGTACCTTACCAGATGTTTGGCAGACATGGGCAACGTCATTGGCTAGAC 1260
|||||
DB 3478 AACGAAATACATTTACCTTACACAGATGTTTGGCAGACATGGGCAACGTCATTGGCTAGAC 3537
QY 1261 CAGAAGGCAAGCAAGAAAGTTAGCTGTCAAAAAAGATATCTCTAGAGGCTTTCCAGANT 1320
|||||
DB 3538 CAGAAGGCAAGCAAGAAAGTTAGCTGTCAAAAAAGATATCTCTAGAGGCTTTCCAGANT 3597
QY 1321 AGTCTCTACCTACGACGACCAATGGGGCAAAATTTACTACTATTGGCATACATTAC 1380
|||||
DB 3598 AGTCTCTACCTACGACGACCAATGGGGCAAAATTTACTACTATTGGCATACATTAC 3657
QY 1381 CAGTAAAGTCTTACACACCACTAACCTGTTGAAGGCTCTCTTGGCCAACGGGTGAG 1440
|||||
DB 3658 CAGTAAAGTCTTACACACCACTAACCTGTTGAAGGCTCTCTTGGCCAACGGGTGAG 3717
QY 1441 AATGACCTAATGAGAGGAGCAACACTTTTTCACCGCTCTACTGCTACATCTCTAGAC 1500
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DB 3718 AATGACCTAATGAGAGGAGCAACACTTTTTCACCGCTCTACTGCTACATCTCTAGAC 3777
QY 1501 GGTGACGGGTGAGTGTGCTTGGCCATGACCGCTGCTGTTGTTGACGACATGGGCAC 1560
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DB 3778 GGTGACGGGTGAGTGTGCTTGGCCATGACCGCTGCTGTTGTTGACGACATGGGCAC 3837
QY 1561 GCTTGCACCGTGAATCACTGACATGACATGCCCCCGCGCTGCGCGGCTACAAAAGCCA 1620
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DB 3838 GCTTGCACCGTGAATCACTGACATGACATGCCCCCGCGCTGCGCGGCTACAAAAGCCA 3897
QY 1621 CACAGCAGCGCGGCGCAACGATACCTCTAGATCCCGGTGTCCAGAAAGATGCCAT 1680
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DB 3898 CACAGCAGCGCGGCGCAACGATACCTCTAGATCCCGGTGTCCAGAAAGATGCCAT 3957
QY 1681 CAAGCCGTGCGCATG 1695
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DB 3958 CAAGCCGTGCGCATG 3972

RESULT 6
AR207455 5349 bp DNA linear PAT 20-JUN-2002
LOCUS AR207455
DEFINITION Sequence 7 from patent US 6372960.
ACCESSION AR207455
VERSION AR207455.1 GI:21506374
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5349)
AUTHORS Michlels, F. and Williams, M.
TITLE Barstar gene
JOURNAL Patent: US 6372960-A 7 16-APR-2002;
FEATURES
source location/Qualifiers
1..5349
BASE COUNT 1339 a 1253 c 1290 g 1487 t
ORIGIN

Query Match 100.0%; Score 1695; DB 6; Length 5349;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCAGATCCTTGTGTGATGTTTATTAAATTTAATATTATCTGGAATACCTACC 60
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DB 2278 CCGCAGATCCTTGTGTGATGTTTATTAAATTTAATATTATCTGGAATACCTACC 2337
QY 61 AATTTATAGTATGAGTGTGCAAGTGCAGAACTTCCAAATGGCGCAATTCATATAGAG 120
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DB 2338 AATTTATAGTATGAGTGTGCAAGTGCAGAACTTCCAAATGGCGCAATTCATATAGAG 2337
QY 121 TCCAGACCACTTAATATCATAAACATCTGATGTTAGTCCAGAACTATTTAGTAGTG 180
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DB 2398 TCCAGACCACTTAATATCATAAACATCTGATGTTAGTCCAGAACTATTTAGTAGTG 2457

QY 181 AACCAATATAGCAATTAACATTTATGAGATTTATGGCTAACTGCAATTCATTTCT 240
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DB 2458 AACCAATATAGCAATTAACATTTATGAGATTTATGGCTAACTGCAATTCATTTCT 2517
QY 241 GATGGCTATATCTGTGTAATTTTATGGCTCCAGAAATAATGGCAATCTCTGGACAT 300
|||||
DB 2518 GATGGCTATATCTGTGTAATTTTATGGCTCCAGAAATAATGGCAATCTCTGGACAT 2577
QY 301 GTTGGCACTGAACTGTGTCATGTTTATACATCTCTTTTAACTAGCAAGAGATAGAT 360
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DB 2578 GTTGGCACTGAACTGTGTCATGTTTATACATCTCTTTTAACTAGCAAGAGATAGAT 2637
QY 361 TATATATACGAGAAATCTCTTACATCTCTTCCATATGCAATGTCGTAAGACAG 420
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DB 2638 TATATATACGAGAAATCTCTTACATCTCTTCCATATGCAATGTCGTAAGACAG 2697
QY 421 ATACAGTACCTGTTGTTGTAATGAGGCTCAATGCCATTTCTGTGAAGCATTTGAG 480
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DB 2698 ATACAGTACCTGTTGTTGTAATGAGGCTCAATGCCATTTCTGTGAAGCATTTGAG 2757
QY 481 AGATGATGATTTCTGGGATCTTGGAGGGCCCTGAAATTCGGAACAGTTAGATT 540
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DB 2758 AGATGATGATTTCTGGGATCTTGGAGGGCCCTGAAATTCGGAACAGTTAGATT 2817
QY 541 TTATGATCTAATGCTTTCGCTTATATCTAGCTAAATGCGATTTCTGTAACTGATTTTC 600
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DB 2818 TTATGATCTAATGCTTTCGCTTATATCTAGCTAAATGCGATTTCTGTAACTGATTTTC 2877
QY 601 TTGCATCTCCAGGAAATTAAGCTAATATCTGTCCAAAGAGTGTGGCATTTGACCA 660
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DB 2878 TTGCATCTCCAGGAAATTAAGCTAATATCTGTCCAAAGAGTGTGGCATTTGACCA 2937
QY 661 ATGAAGATCAAGCATGGCAAGATGGCAATCTGCAAAAGGACGGAAATTAATTTAT 720
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DB 2938 ATGAAGATCAAGCATGGCAAGATGGCAATCTGCAAAAGGACGGAAATTAATTTAT 2997
QY 721 TCTACTACATCCAGAGAACCATATCAATGTTGCCCAAGAGACCCCGCATATTAAG 780
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DB 2998 TCTACTACATCCAGAGAACCATATCAATGTTGCCCAAGAGACCCCGCATATTAAG 3057
QY 781 TTCCGTGTTTCCACAGCAAGATATCCGCAATGATACCTCCCAACATGAAATCCAA 840
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DB 3058 TTCCGTGTTTCCACAGCAAGATATCCGCAATGATACCTCCCAACATGAAATCCAA 3117
QY 841 ACCACATCGGCTCAGAGAGATGATGATAAAGGCATTAATTTGATTAATTTCTTGA 900
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DB 3118 ACCACATCGGCTCAGAGAGATGATGATAAAGGCATTAATTTGATTAATTTCTTGA 3177
QY 901 AAGCGAATTAATATACACCTTGACCTCCACCAAGAGCTTGGGATCGACTGTGCC 960
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DB 3178 AAGCGAATTAATATACACCTTGACCTCCACCAAGAGCTTGGGATCGACTGTGCC 3237
QY 961 CATGAATGGCATTTGACATCTGCTCACTGTCAGAAATCTCTCGGAAATGAGAGGCA 1020
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DB 3238 CATGAATGGCATTTGACATCTGCTCACTGTCAGAAATCTCTCGGAAATGAGAGGCA 3297
QY 1021 TAGCTTGTGTGTGTATGTGTGTGGGATTAATGCTGTCTTAAACCTTGTGTTCTGATG 1080
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DB 3298 TAGCTTGTGTGTGTATGTGTGTGGGATTAATGCTGTCTTAAACCTTGTGTTCTGATG 3357
QY 1081 ATCTGTTGAGAGCATGCGCTTATAGACACTTAAATAATGGTATGATTAATCTCAAG 1140
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DB 3358 ATCTGTTGAGAGCATGCGCTTATAGACACTTAAATAATGGTATGATTAATCTCAAG 3417
QY 1141 AGCCTATACCTGCAAGAAAGATAGCTTGGCTGTGGGATTTGAGCCGCTTGAAGGAAC 1200
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DB 3418 AGCCTATACCTGCAAGAAAGATAGCTTGGCTGTGGGATTTGAGCCGCTTGAAGGAAC 3477
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DB 3478 AAGCAATATGATTTACCTTACAGATGTTTGGCAACATGGGCAACGTCATTTGTAAG 3537

Db 3227 ATCTGTTAGAGAGCATCGTCTTTATAGCAGCTTAAATGGTAGATATATCTCTCAAG 3168
QY 1141 ACCCTATCTGCCAAGAAAGATAGCTGGCCCTGTGGGATTTAGCCCTTGAAGGAAAC 1200
Db 3167 AGCCTATCTGCGCAAGAAAGATAGCTGGCCCTGTGGGATTTAGCCCTTGAAGGAAAC 3108
QY 1201 AAGCAATACAGTTACCTTACAGATGTTTTCAGCAGCATGGCAAGCTCATCTTCTAGAC 1260
Db 3107 AATGCAATACAGTTACCTTACAGATGTTTTCAGCAGCATGGCAAGCTCATCTTCTAGAC 3048
QY 1261 CAGAAGGCAAGAAAGATTACCTCTCAAAAAGATATGCTAGAGAGCTTTCTCAGAAAT 1320
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QY 1441 AATGCACTAATGAGCGGAGCAACACTTCTTCAACGCTCTACTGCTACATCTGTAGAC 1500
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QY 1501 GGTGAGCGGTGAGGCTTGTGGCCATGACCGTCTTGTGTGTGAGACTTGGCCAC 1560
Db 2807 GGTGAGCGGTGAGGCTTGTGGCCATGACCGTCTTGTGTGTGAGACTTGGCCAC 2748
QY 1561 GCTTGACAGCTGACCTACCTGCAATGACCGCCGCGCGGCGGCGCTCAAAAAGCCA 1620
Db 2747 GCTTGACAGCTGACCTACCTGCAATGACCGCCGCGCGGCGGCGCTCAAAAAGCCA 2688
QY 1621 CACAGCAGCGCGGCGCCAGCAATGACCGCTTGTGTGTGAGACTTGGCCAC 1680
Db 2687 CACAGCAGCGCGGCGCCAGCAATGACCGCTTGTGTGTGAGACTTGGCCAC 1628
QY 1681 CAAGCGCTGCGGATG 1695
Db 2627 CAAGCGCTGCGGATG 2613

RESULT 8
LOCUS A60109 6548 bp DNA circular PAT 22-OCT-1999
DEFINITION Sequence 2 from Patent W09706267.
ACCESSION A60109
VERSION A60109.1 GI:3715125
KEYWORDS Plasmid pTS172.
SOURCE Plasmid pTS172
ORGANISM plasmids.
REFERENCE 1 (bases 1 to 6548)
AUTHORS De B.M.
TITLE Genetic transformation using a PARP inhibitor
JOURNAL Patent: WO 9706267-A 2 20-FEB-1997;
PLANT GENETIC SYSTEMS NY (BE)
FEATURES
source
1. 6548
/organism="Plasmid pTS172"
/db_xref="taxon:106340"
BASE COUNT 1756 a 1579 c 1523 g 1690 t
ORIGIN

Query Match 100.0%; Score 1695; DB 6; Length 6548;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCAGATCTCTTGTGCTGATGTTTATTAATAATATTATTCGAACTACAC 60
Db 4316 CCGCAGATCTCTTGTGCTGATGTTTATTAATAATATTATTCGAACTACAC 4257

QY 61 AATATATAGAGAGCTTGTCAAGCTGCAAGAACTTCCAAATCCCGGCAATACCAATAGAGA 120
Db 4256 AATATATAGAGAGCTTGTCAAGCTGCAAGAACTTCCAAATCCCGGCAATACCAATAGAGA 4197
QY 121 TCCAGCCAGCTTAAATATCATTAACAAATCTGATTTAGTCCAGAACTATTTGAGTAGTG 180
Db 4196 TCCAGCCAGCTTAAATATCATTAACAAATCTGATTTAGTCCAGAACTATTTGAGTAGTG 4137
QY 181 AACACAATAGCAATTAACATTTATAGATTTATGGCTTAACCTGCAATTCATATTCCT 240
Db 4136 AACACAATAGCAATTAACATTTATAGATTTATGGCTTAACCTGCAATTCATATTCCT 4077
QY 241 GATCGCTAATCTGATCAATTTAGCGCTCCAGAAAGAAATTCGCAATCTTGGACAT 300
Db 4076 GATCGCTAATCTGATCAATTTAGCGCTCCAGAAAGAAATTCGCAATCTTGGACAT 4017
QY 301 GTTGGCACTGGAACCTGTTGCATGTTTATCATCTCTTATTAACGTACCAAGAGTAGAT 360
Db 4016 GTTGGCACTGGAACCTGTTGCATGTTTATCATCTCTTATTAACGTACCAAGAGTAGAT 3957
QY 361 TATATATACAGAGAAATCTCTTCAGATCTTTCACATGCAATGCTTAAAGAACG 420
Db 3956 TATATATACAGAGAAATCTCTTCAGATCTTTCACATGCAATGCTTAAAGAACG 3897
QY 421 ATACAGTACGTTAGTGTGTAATGAGAGGCTCAATGCCATTTCTGTAAGGATGTTAG 480
Db 3896 ATACAGTACGTTAGTGTGTAATGAGAGGCTCAATGCCATTTCTGTAAGGATGTTAG 3837
QY 481 AGATGATGATTTCTGAGATCTCTTGAAGGCGCCCTGAAATTCGGAAGAGTTAGTTGAGTT 540
Db 3836 AGATGATGATTTCTGAGATCTCTTGAAGGCGCCCTGAAATTCGGAAGAGTTAGTTGAGTT 3777
QY 541 TTAATACCTAATGCTCTGCTGATTAATACGTGAATGCAATTTCTGTAAGCTGAGTTTC 600
Db 3776 TTAATACCTAATGCTCTGCTGATTAATACGTGAATGCAATTTCTGTAAGCTGAGTTTC 3717
QY 601 TACATCTCCAGAGAAATTAAGCTAATACCTGTCAGAGAGGCGGAGCTTGGACCA 660
Db 3716 TACATCTCCAGAGAAATTAAGCTAATACCTGTCAGAGAGGCGGAGCTTGGACCA 3657
QY 661 ATGAAGATCAAGAGATGGCAGAAATGCGCAATCTGCAAGAGAGCGCAATTAATGTTAT 720
Db 3656 ATGAAGATCAAGAGATGGCAGAAATGCGCAATCTGCAAGAGAGCGCAATTAATGTTAT 3597
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Db 3596 TCTACTACATCGAAGAGAACCATATCATGTTGCCCGCAGAGAGACCCCGCAGATAG 3537
QY 781 TTCTGTTCTTCCACAGCAGAAATATCCGCAACTGATAGCTGCCAAGCAATGAATCCAA 840
Db 3536 TTCTGTTCTTCCACAGCAGAAATATCCGCAACTGATAGCTGCCAAGCAATGAATCCAA 3477
QY 841 ACCAGATCGCTCAGAGAGAAATTAATGAATGAAGCATAATTCGAATTAATTCCTAGA 900
Db 3476 ACCAGATCGCTCAGAGAGAAATTAATGAATGAAGCATAATTCGAATTAATTCCTAGA 3417
QY 901 AAGCAATTAATTAACACACCTGAGCTGACCAAGAAAGCTGTGGATGAGTATGCTGGC 960
Db 3416 AAGCAATTAATTAACACACCTGAGCTGACCAAGAAAGCTGTGGATGAGTATGCTGGC 3357
QY 961 CATGAATATGCAATCTGACATTTCTGCTACTGTCAGATCTCTGGAATAATGAGAGGCA 1020
Db 3356 CATGAATATGCAATCTGACATTTCTGCTACTGTCAGATCTCTGGAATAATGAGAGGCA 3297
QY 1021 TAGCTTCTGCTGATGATGTTGTTGGATTAATACGCTGTAACCTTGTGTTCTGATG 1080
Db 3296 TAGCTTCTGCTGATGATGTTGTTGGATTAATACGCTGTAACCTTGTGTTCTGATG 3237
QY 1081 ATCGGTTAGAGAGCATGCTTTATTAAGCATTAAATATGATTAATCTCTCAAG 1140
Db 3236 ATCGGTTAGAGAGCATGCTTTATTAAGCATTAAATATGATTAATCTCTCAAG 3177
QY 1141 AGCTATACCTGCCAAGAAAGATAGCTTGGCTGTGGGATGTAGCCGTTGAAGGAAC 1200

OY 1201 AAAGCAATACGATTACCTTACAGATGTTTGGCAGACGAGGACGTCATTCGTAGAC 1260
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Db 3116 AAACGAATACGATTACCTTACAGATGTTTGGCAGACGATGGCAAGCTCATTCGTAGAC 3037
OY 1261 CAAGAGGCAAGCAAGCAAGTTTACCTGTCACAAAAGATATGTAGAGGCTTTCCAGAAAT 1320
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Db 3056 CAAGAGGCAAGCAAGCAAGTTTACCTGTCACAAAAGATATGTAGAGGCTTTCCAGAAAT 2997
OY 1331 ATGTTCTATCTCAGCAGACCAATGGGGGCAAAATTTACTACTATTTGCCATTCATTAC 1380
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Db 2996 ATGTTCTATCTCAGCAGACCAATGGGGGCAAAATTTACTACTATTTGCCATTCATTAC 2937
OY 1381 CACGTAAGAGCTTACATCTCAACCTAATGTTGAAGGCTGCTGTTCCGCAAGGCTGAG 1440
|||||
Db 2936 CACGTAAGAGCTTACATCTCAACCTAATGTTGAAGGCTGCTGTTCCGCAAGGCTGAG 2877
OY 1441 AATGCACTTATGTAGAGGCAAGCAACTCTTTTCAACCGTACTGCTCATCTGTAGAC 1500
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Db 2876 AATGCACTTATGTAGAGGCAAGCAACTCTTTTCAACCGTACTGCTCATCTGTAGAC 2817
OY 1501 GGTGAGCGCTGAGGTGCTTTGCCATGACCGTCTTGGTTGTGACGTCACTTGCAGAC 1560
|||||
Db 2816 GGTGAGCGCTGAGGTGCTTTGCCATGACCGTCTTGGTTGTGACGTCACTTGCAGAC 2757
OY 1561 GCTTGACCGCTGACCTCAGCTGCAATGTCCTGCGCCGCTGCGCGGCGCTTACAAAGCA 1620
|||||
Db 2756 GCTTGACCGCTGACCTCAGCTGCAATGTCCTGCGCCGCTGCGCGGCGCTTACAAAGCA 2697
OY 1621 CACAGCAGCGCGGCGGCAAGTAAACCATCTAGATCCCGGCTGTCAGCAGAGATCCAT 1680
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Db 2696 CACAGCAGCGCGGCGGCAAGTAAACCATCTAGATCCCGGCTGTCAGCAGAGATCCAT 2637
OY 1681 CAAGCGCTGCGGATG 1695
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Db 2636 CAAGCGCTGCGGATG 2622

RESULT 10
AR098308/c AR098308 6548 bp DNA linear PAT 14-FEB-2001
- LOCUS Sequence 2 from patent us 6074876.
DEFINITION AR098308
ACCESSION AR098308.1 GI:12807565
VERSION AR098308.1 GI:12807565
KEYWORDS
SOURCE
ORGANISM
Unknown.
unclassified.
REFERENCE
1 (bases 1 to 6548)
AUTHORS De Block M.
TITLE Genetic transformation using a PAPR inhibitor
JOURNAL Patent: US 6074876-A 2 13-JUN-2000;
FEATURES
source 1..6548
/organism="unknown"
BASE COUNT 1756 a 1579 c 1523 g 1690 t
ORIGIN

Query Match 100.0%; Score 1695; DB 6; Length 6548;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGGAGATCCTTCTGTGTGATGTTTAAATTTAAATTTATTTATCTGGAATACCTAC 60
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Db 4316 CCGGAGATCCTTCTGTGTGATGTTTAAATTTAAATTTATTTATCTGGAATACCTAC 4257
OY 61 AATATATGTAGTACCTGTCAGAGCTGCAAGAACTTCCAAATGCGCGCAATPACCAATAGGA 120
|||||
Db 4256 AATATATGTAGTACCTGTCAGAGCTGTCAGAACTTCCAAATGCGCGCAATPACCAATAGGA 4197
OY 121 TCCAAACCACTTAAATATCATTAACAATCATGATTTAGTCCAGAACTATTTAGTAGTG 180
|||||
Db 4196 TCCAAACCACTTAAATATCATTAACAATCATGATTTAGTCCAGAACTATTTAGTAGTG 4137

OY 181 AACACAATAGCACATTACATTTAGAGATTAATGCTTAAGCTGCAATTCATATTC 240
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Db 4136 AACACAATAGCACATTACATTTAGAGATTAATGCTTAAGCTGCAATTCATATTC 4077
OY 241 GATCGCTATATCTGTCATATTTAGCGCTCCAGAAAGAAATTCACAAATCCTTGACAAAT 300
|||||
Db 4076 GATCGCTATATCTGTCATATTTAGCGCTCCAGAAAGAAATTCACAAATCCTTGACAAAT 4017
OY 301 GTTGCGCACTGGAAGCTGTTGCAATGTTTTTACATCTCTTTATTTAGCTAGCAAGAGTAGAT 360
|||||
Db 4016 GTTGCGCACTGGAAGCTGTTGCAATGTTTTTACATCTCTTTATTTAGCTAGCAAGAGTAGAT 3957
OY 361 TATATATACAGAGAAATCTCTTCAGATCCCTTCCACATTCGCAATGCTGTAAGAACAG 420
|||||
Db 3956 TATATATACAGAGAAATCTCTTCAGATCCCTTCCACATTCGCAATGCTGTAAGAACAG 3897
OY 421 ATACAGTGTAGCTAGTTTGTAAATGAGCGGTCAATGTCATTTCTCTGAAAGCATGTTGAG 480
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Db 3896 ATACAGTGTAGCTAGTTTGTAAATGAGCGGTCAATGTCATTTCTCTGAAAGCATGTTGAG 3837
OY 481 AGATGATGATTTTGGGATCCTTGAGAGGCGCTGAAATTCGCAAGCATTTAGTTGAGTT 540
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Db 3836 AGATGATGATTTTGGGATCCTTGAGAGGCGCTGAAATTCGCAAGCATTTAGTTGAGTT 3777
OY 541 TTACTACTATATCTCTCCCTTATACATGAGTAAATGCAATTCCTGTAAGCTGAGTTTC 600
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Db 3776 TTACTACTATATCTCTCCCTTATACATGAGTAAATGCAATTCCTGTAAGCTGAGTTTC 3717
OY 601 TACATCTCCACAGAAATTAAGCTTAATACCTGTCACAAAGATGTTGGGATTTGACCA 660
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Db 3716 TACATCTCCACAGAAATTAAGCTTAATACCTGTCACAAAGATGTTGGGATTTGACCA 3657
OY 661 ATGAGATCAGCAAGCATGCAAGAAATGGCAATTCGGCAAGAGCGGCAATTTATTTGTAT 720
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Db 3656 ATGAGATCAGCAAGCATGCAAGAAATGGCAATTCGGCAAGAGCGGCAATTTATTTGTAT 3597
OY 721 TCTACTATATGAAACAGAACCATATCATGTTGCCCGAGAAAGAGCGCGGATTAAG 780
|||||
Db 3596 TCTACTATATGAAACAGAACCATATCATGTTGCCCGAGAAAGAGCGCGGATTAAG 3537
OY 781 TTCTGTTCTTCCACAGAGAAATTCGCAACATGATAGCTCCCAACAAATGAAATCCCAA 840
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Db 3536 TTCTGTTCTTCCACAGAGAAATTCGCAACATGATAGCTCCCAACAAATGAAATCCCAA 3477
OY 841 ACCACATCGGCTCAGAGAGAAATTAAGCACTAATTTCTGAATTAATTTCTAGA 900
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Db 3476 ACCACATCGGCTCAGAGAGAAATTAAGCACTAATTTCTGAATTAATTTCTAGA 3417
OY 901 AAGCAATTAATTAAGCAACACCTTGACCTCCACCAAGAGCTTGATGACCTTGAGCC 960
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Db 3416 AAGCAATTAATTAAGCAACACCTTGACCTCCACCAAGAGCTTGATGACCTTGAGCC 3357
OY 961 CATGAATGCGATTTCTGACATTTCTGTCAGTCTGAGATCTCTCGGAAATGAGAGGCA 1020
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Db 3356 CATGAATGCGATTTCTGACATTTCTGTCAGTCTGAGATCTCTCGGAAATGAGAGGCA 3297
OY 1021 TAGCTTCTGTGTATGTGTGCGGATTAATGCTGCTAAACTTTGTGTGATCG 1080
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Db 3296 TAGCTTCTGTGTATGTGTGCGGATTAATGCTGCTAAACTTTGTGTGATCG 3237
OY 1081 ATTCGTTAGAGAGCATGCTTTAATTAAGCACTTAATTAATGCTGTAATTCCTGCAAG 1140
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Db 3236 ATTCGTTAGAGAGCATGCTTTAATTAAGCACTTAATTAATGCTGTAATTCCTGCAAG 3177
OY 1141 AGCTATATCTCCAGAGAAAGATAGCTTGGCTGTGGGATTAAGCGTTGAGAGGGAAC 1200
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Db 3176 AGCTATATCTCCAGAGAAAGATAGCTTGGCTGTGGGATTAAGCGTTGAGAGGGAAC 3117
OY 1201 AAACGAATACAGTTACCTTACCAAGATGTTTGCAGCAGATGGGCAACGTCATTCAGAC 1260
|||||
Db 3116 AAACGAATACAGTTACCTTACCAAGATGTTTGCAGCAGATGGGCAACGTCATTCAGAC 3057
OY 1261 CAAGAGGCAAGCAAGCTTATAGCTGTCAAAAAAGATATGCTAGAGGCTTTCCACAAT 1320

Db	3056	CAGGAAGCGAAGACCAAGTTTAGTGTGCAAAAAAGATATCTGAGGCTTTCCAGAAAT	2997
Qy	1321	ATGTTCTATCTCAGCGACAGACCAATGGGGGCAAAATTTACTACTATTTGGCATACATTAAC	1380
Db	2996	ATGTTCTATCTCAGCGACAGACCAATGGGGGCAAAATTTACTACTATTTGGCATACATTAAC	2937
Qy	1381	CACGTAAGAGTCCCTACACTCAACTTAACCTGTTGAAGCGTCTGTTGTGCCCAAGGTGAG	1440
Db	2936	CACGTAAGAGTCCCTACACTCAACTTAACCTGTTGAAGCGTCTGTTGTGCCCAAGGTGAG	2877
Qy	1441	AATGCACCTTAATGAGACGGGACAACACTTCTTTACCGTGTACTCCTACATCTGTAGAC	1500
Db	2876	AATGCACCTTAATGAGACGGGACAACACTTCTTTACCGTGTACTCCTACATCTGTAGAC	2817
Qy	1501	GGTGGACGGGTAGAGTGCTTTTGGCCATGACGTCCTTGGTTTGACATCTTGGCGAC	1560
Db	2816	GGTGGACGGGTAGAGTGCTTTTGGCCATGACGTCCTTGGTTTGACATCTTGGCGAC	2757
Qy	1561	GGTTGCACCGGTAGACCTTGGCCATGACGTCCTTGGTTTGACATCTTGGCGAC	1620
Db	2756	GGTTGCACCGGTAGACCTTGGCCATGACGTCCTTGGTTTGACATCTTGGCGAC	2697
Qy	1621	CACAGCGACGGCGGACAGATTAACCATCTAGATCCGGGTGTCCAGCAAGATTCAT	1680
Db	2696	CACAGCGACGGCGGCGACAGATTAACCATCTAGATCCGGGTGTCCAGCAAGATTCAT	2637
Qy	1681	CACGCGTTCGCGATG 1695	
Db	2636	CACGCGTTCGCGATG 2622	

RESULT 11					
LOCUS	E31990/c				
DEFINITION	Mutated barnase gene and transgenic plant thereof.	6548 bp	DNA	linear	PAT 18-JUN-2001
ACCESSION	E31990				
VERSION	E31990.1	GI:13021587			
KEYWORDS	JP 2000041682-A/3.				
SOURCE	unidentified.				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 6548)				
AUTHORS	Kazuyuki, H. and Fumio, N.				
TITLE	Mutated barnase gene and transgenic plant thereof				
JOURNAL	Patent: JP 2000041682-A 3 15-FEB-2000;				
	JAPAN TOBACCO INC				
COMMENT	OS Escherichia coli LE392				
	PN JP 2000041682-A/3				
	PD 15-FEB-2000				
	PF 04-NOV-1998 JP 1998220060				
	PR				
	PI KAZUYUKI HAMADA, FUMIO NAKAKIDO				
	PC C12N15/09, A01H5/00, C12N5/10, C12N9/22//C12N5/10, C12R1:91), PC				
	C12N15/00,				
	PC C12N5/00, (C12N5/00, C12R1:91)				
FEATURES					
SOURCE					
FT	key	Location/Qualifiers			
FT	source	1..6548			
FT		/organism='Escherichia coli LE392'.			
	location/Qualifiers	1..6548			
		/organism='unidentified'			
		/db_xref='taxon:32644'			
BASE COUNT	1756 a 1579 c 1523 g 1690 t				
ORIGIN					

Query Match	100.0%	Score 1695;	DB 6;	Length 6548;
Best local Similarity	100.0%	Pred. No. 0;		
Matches 1695;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CCGCAGATCCCTTCGTGTGATGATGTTTAAATTAATTTATCTGCAATACCTACC	60	

Db	4316	CCGAGATCCCTTCGTGCTGATGTTTATTAAATTAAATTATCTGGAAATACCTACC	4257
Qy	61	AATATATAGTAGACTGTGGCAAGCGCAAGAACTTCCAAATCGCGCAATACCAATAGAGA	120
Db	4256	AATATATAGTAGACTTGTCAAGCTGCAGAAACTTCCAAATGCGGACAAATACCAATAGAGA	4197
Qy	121	TCCAACCACTTAATATCATAAACAATCTAAATGTTAGTCCAGAACTATATAGCACTAG	180
Db	4136	TCCAACCACTTAATATCATAAACAATCTAATGTTAGTCCAGAACTATATAGCACTAG	4137
Qy	181	AACAACATAGCACATTACATTAATAGAGATTAATGGCTACCTGCACATTCATTAATCT	240
Db	4136	AACAACATATACACATTACATTAATAGAGATTAATGGCTACCTGCACATTCATTAATCT	4077
Qy	241	GATGGTCTAATCTGGTCAATTTTAAAGCGCTCCAGAAAGATTGCACAATCCTTGGACAT	300
Db	4076	GATGGTCTAATCTGGTCAATTTTAAAGCGCTCCAGAAAGATTGCACAATCCTTGGACAT	4017
Qy	301	GTTGGCACTGGAACCTGTTGCATGTTTTACATCTCTTAATTAACGTAGCAAAAGAGTAGAT	360
Db	4016	GTTGGCACTGGAACCTGTTGCATGTTTTACATCTCTTAATTAACGTAGCAAAAGAGTAGAT	3957
Qy	361	TATATATGACAGAGAGAAATCTCTCAGATCCTTTCCACATGCAATGTCTGTAAGAACAG	420
Db	3956	TATATATGACAGAGAGAAATCTCTCAGATCCTTTCCACATGCAATGTCTGTAAGAACAG	3897
Qy	421	ATACAGTGTACGTAGTTTCTTAATGCAAGCGTCAATGCCATTTCTCTGAAGGATGTTAG	480
Db	3896	ATACAGTGTACGTAGTTTCTTAATGCAAGCGTCAATGCCATTTCTCTGAAGGATGTTAG	3837

Db	3836	AGATGATGATTTTCGGGATCCTTGGAGGGGCCCTGAAATTCGGAAACAGTTAGTTGAGTT	3777
Qy	541	TTAGACTTAATGTCCTGGCTGTAATACAGTGAAGAAAGCATTTCTGTAAAGCGAGTTTC	600
Db	3776	TTAGTACCTAATGCTTGCTGCTTATCTAGCTGAATGCGATTTCGTAGCTGAGTTTC	3717
Qy	601	TAGCATCTCCACAGAAATAAAGCTAATACCTGTCCAAAGTGGTGCGGCAATTTGACCA	660
Db	3716	TACCATCTCCACAGAAATAAAGCTAATACCTGTCCAAAGTGGTGCGGCAATTTGACCA	3657
Qy	661	ATGAAATGCACAAAGCATGGGAAGAATGGCAATCTGGCAAGAGCGGGAATATATTGAT	720
Db	3656	ATGAAATGCACAAAGCATGGGAAGAATCTGGCAAGAGCGGGAATATATTGAT	3597
Qy	721	TCTACTCATGCAACAGAGACCATATTCATGTTGGCCCGCAGAGACCCCGCAGATAG	780
Db	3596	TCTACTCATGCAACAGAGACCATATTCATGTTGGCCCGCAGAGACCCCGCAGATAG	3537
Qy	781	TTCTGTTCTTCCACAGCAGAAATATCCGACACTAGCTCCCAACAAATGCAATCCAA	840
Db	3536	TTCTGTTCTTCCACAGCAGAAATATCCGACACTAGCTCCCAACAAATGCAATCCAA	3477
Qy	841	ACGCATCGGCTCAGAGAGAGATTGATTAAGTAAGACACATAATTCGATTAATTTCCAGA	900
Db	3476	ACGCATCGGCTCAGAGAGAGATTGATTAAGTAAGAGCACATAATTCGATTAATTTCCAGA	3417
Qy	901	AAGGATTAATTAATACACACACTTGACACTGCCAACAAAGAGTTGGATGCACTTGTGCC	960
Db	3416	AAGGATTAATTAATACACACACTTGACACTGCCAACAAAGAGTTGGATGCACTTGTGCC	3357
Qy	961	CATCAANTGCAATTCGACATTCCTGCTCAGATTCCTCGGAATAAGAGAGCA	1020
Db	3356	CATCAANTGCAATTCGACATTCCTGCTCAGATTCCTCGGAATAAGAGAGCA	3297
Qy	1021	TAGCTTCGTGTGATGATGATGGGGAATTTACGCTCGCTAAACCTGTTGTTGATGTCG	1080
Db	3296	TAGCTTCGTGTGATGATGATGGGGAATTTACGCTCGCTAAACCTGTTGTTGATGTCG	3237
Qy	1081	ATCGCTTACAGAGCATCCTCTTTTAATAGCACTTTAAATAAGTATGATTAATCTCCAGG	1140
Db	3236	ATCGCTTACAGAGCATCCTCTTTTAATAGCACTTTAAATAAGTATGATTAATCTCCAGG	3177

Oy	1141	AGGATATCTGTCCGAAGAAAGGATTGGCTTGGCGTGGGGATTGGACGGTTGAAAGGAAAC	1200
Oy	1201	AAMCGAATACAGTTACTTTCACAGATGTTTTGCCACGCATGGCAACTCATTTGCTTAGAC	1260
Db	3176	AGCCTATCTACTCCAGAAGAAAGATAGCTTGGCCGTGGGGATTGAGCCGTTGAAAGGAAAC	3117
Oy	1201	AAMCGAATACAGTTACTTTCACAGATGTTTTGCCACGCATGGCAACTCATTTGCTTAGAC	1260
Db	3116	AAMCGAATACAGTTACTTTCACAGATGTTTTGCCACGCATGGCAACTCATTTGCTTAGAC	3057
Oy	1261	CAGAAGGCCAAGAACGAAGTTAGCTGTCAAAAAACATATPCTTAGAGGCTTTCCAGAAAT	1320
Db	3056	CAGAAGGCCAAGAACGAAGTTAGCTGTCTCAAAAAACATATGCTTAGAGGCTTTCCAGAAAT	2997
Oy	1321	ATGTTCTATCTCACGCCAGACCAATGGGGGGCAAATTTACTACATAATTTGCCATTAATTAC	1380
Db	2996	ATGTTCTATCTCACGCCAGACCAATGGGGGGCAAATTTACTACATAATTTGCCATTAATTAC	2937
Oy	1381	CACGTAAAGATCTCACACTCAACCTTCACTGTTGAAAGGATCTGTTTCTGGCCAAGGGTAG	1440
Db	2936	CACGTAAAGATCTCACACTCAACCTTCACTGTTGAAAGGATCTGTTTCTGGCCAAGGGTAG	2877
Oy	1441	AATGCACCTAATGAGACGGGACAACACTCTTTCACGCGTGTACGTCTACATCCGTATGAC	1500
Db	2876	AATGCACCTAATGAGACGGGACAACACTCTTTCACGCGTGTACGTCTACATCCGTATGAC	2817
Oy	1501	GGTGCACGCGTGAGAGTGCTTTGCCATFACACCCTGTTGGTTGTGCAATCACTTGGGCAC	1560
Db	2816	GGTGCACGCGTGAGAGTGCTTTGCCATFACACCCTGTTGGTTGTGCAATCACTTGGGCAC	2757
Oy	1561	GCTTGCACCGGTGACTCACTGTCACAAATTTGGCCCCCGCGTGCACGGCGCTACAAAACCA	1620
Db	2756	GCTTGCACCGGTGACTCACTGTCACAAATTTGGCCCCCGCGTGCACGGCGCTACAAAACCA	2697
Oy	1621	CACACGCAAGCGCGGCGCCAGATAACCATCTAGCATCCCGGTGTCCACAGAGATTCAT	1680
Db	2696	CACACGCAAGCGCGGCGCCAGATAACCATCTAGCATCCCGGTGTCCACAGAGATTCAT	2637
Oy	1681	CAGCGGTGCGGATG 1695 	
Db	2636	CAGCGGTGCGGATG 2622 	
RESULT 12			
BD013094/c			
LOCUS	BD013094	7492 bp	DNA
DEFINITION	Method for producing male-sterile plant.		Linear
VERSION	BD013094		PAT 02-AUG-2002
KEYWORDS	WO 0124616-A/5. synthetic construct. artificial sequences.		
SOURCE	ORGANISM		
REFERENCE	Hameda,K. and Nakajido,F. Title Journal		
COMMENT	Method for producing male-sterile plant Patent: WO 0124616-A 5 12-APR-2001; JAPAN TOBACCO INC. KANUYUKI HAMADA, FUMIO NAKAJIDO OS Artificial Sequence PN WO 0124616-A/5 PD 12-APR-2001 PR 12-SEP-2000 WO 2000JP006222 PF 30-SEP-1999 JP 99P 279307 PI KAZUTOKU HAMADA, FUMIO NAKAJIDO PC A01H5/00,C12N15/11,C12N15/63,C12N15/82 CC Plasmid pHS346 FH Key Location/Qualifiers. source Location/Qualifiers 1..7492 /organism="synthetic construct" /db_xref="taxon:32630"		
BASE COUNT	1987 a	1801 c	1752 g 1952 t
ORIGIN			

[illegible]

D	b	4222	TAGCTTCGATGTGGTATGTGTGCAGATTATACCGTGCTAAACAATTGTGTGTCTGATCG	4163
O	y	1081	ATCAGGTTGACAGCATGCGTCTTTATTAAGCACTAATAAATGGTAGTATTAATCTGTCAAG	1140
D	b	4162	ATCTGGTATGAAGAGATGCTTTTATTAGACTTTAAAATGGTAGTATTAATCTGTCAAG	4103
O	y	1141	AGCCTATACTGCCAAGAAGATAGCTGGCCGTGGGATTAGCCGTTGAAGGAAC	1200
D	b	4102	AGCCTATACTGCCAAGAAGATAGCTGGCCGTGGGATTAGCCGTTGAAGGAAC	4043
O	y	1201	AACGAATACAGTTACCTTTACCAGATGTTTTGCCACAGACANTGGGCAACGTCATTGCTAGAC	1260
D	b	4042	AACGAATACAGTTACCTTTACCAGATGTTTTGCCACAGACANTGGGCAACGTCATTGCTAGAC	3983
O	y	1261	CAGAAGACCAACAAACAAAGTTTACGTCGCAAAAAAAGATATGCTAGAGCGTTTCCAGAA	1320
D	b	3982	CAGAAGACCAACAAACAAAGTTTACGTCGCAAAAAAAGATATGCTAGAGCGTTTCCAGAA	3923
O	y	1321	ATGTCTATCTAGCCAGAACCAATGGGGGCAAAATTTACTACTATTTGGCATTAATTAAC	1380
D	b	3922	ATGTCTATCTAGCCAGAACCAATGGGGGCAAAATTTACTACTATTTGGCATTAATTAAC	3863
O	y	1381	CAGCTAAAGCTTACACTCAACCTAAGTGTGAACGGCTGTCTTGTGGCAACGGGTAG	1440
D	b	3862	CAGCTAAAGCTTACACTCAACCTAAGTGTGAACGGCTGTCTTGTGGCAACGGGTAG	3803
O	y	1441	AATGCACCTAATGACGGGCAACACACTTCTTTCACCGGTGACGTACATCTCTGTAGAC	1500
D	b	3802	AATGCACCTAATGACGGGCAACACACTTCTTTCACCGGTGACGTACATCTCTGTAGAC	3743
O	y	1501	GGTGGACGGGTAGGTGCTTTGGCGCAATGACGGCTGTGGTGTGGCAAGTCACTGTGGCAC	1560
D	b	3742	GGTGGACGGGTAGGTGCTTTGGCGCAATGACGGCTGTGGTGTGGCAAGTCACTGTGGCAC	3683
O	y	1561	GCTTGCACCGTACTCACTCTGSCAATTGCCCCCGCGCTGGCGGGGACCTTCAAAAAGCCA	1620
D	b	3682	GCTTGCACCGTACTCACTCTGSCAATTGCCCCCGCGCTGGCGGGGACCTTCAAAAAGCCA	3623
O	y	1621	CACAGCAGCGCGGACAGATTAACCCATCTAGATTCGCCGGTGTCCAGCAAGAGATTCAT	1680
D	b	3622	CACAGCAGCGCGGACAGATTAACCCATCTAGATTCGCCGGTGTCCAGCAAGAGATTCAT	3563
O	y	1681	CAAGCCGTGGCGATG 1695	
D	b	3562	CAAGCCGTGGCGATG 3548	
<hr/>				
RESULT 13				
BD010122/c				
ID	BD010122	standard; DNA: SYN: 7492 BP.		
XX	BD010122:			
AC	BD010122.1			
XX	SV			
DT	08-FEB-2002 (Rel. 70, Created)			
DT	08-FEB-2002 (Rel. 70, Last updated, Version 1)			
XX				
DE	Method for producing male-sterile plant.			
XX	JP 03075934-T/5.			
KW				
XX				
OS	synthetic construct.			
OC	artificial sequence.			
XX	(1)			
RN	1-7492			
RT	Hamaoka K., Nakakido F.:			
RL	Method for producing male-sterile plant".			
XZ	Patent number JP03075934-T/5, 16-MAR-2001.			
	JAPAN TOBACCO INC.,KAZUYUKI HAMADA,FUMIO NAKAKIDO.			

	CC	OS	Artificial Sequence
	CC	PN	JP_03075934-T/5
	CC	PR	16-MAR-2001
	CC	PF	12-SEP-2000 JP_2000006222
	CC	PR	30-SEP-1999 JP_99P_279307
	CC	PI	KAZUYUKI HAMADA, FUMIO NAKAKIDO
	CC	PC	A01H5/00, C12N15/11, C12N15/63, C12N15/82
	CC	CC	
	CC	CC	
	CC	FT	Key Location/Qualifiers
	CC	FT	/organism="Artificial Sequence"
	XX	XX	
	FH	FH	Key Location/Qualifiers
	FT	FT	source 1..7492
	FT	FT	/db_xref="taxon:32630"
	XX	XX	/organism="synthetic construct"
SQ	Sequence 7492 BP, 1987 A; 1801 C; 1752 G; 1952 T; 0 other:		
	Query Match 100.0%; Score 1695; DB 23; Length 7492;		
	Best Local Similarity 100.0%; Pred. No. 0;		
	Matches 1695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	1	CCCCAGATCCTTGTGTCGATGTTTATTATTAATAATTTATCTGAACTACAC	60
DB	5242	CCCAGATTCCTTGTCGTGATGGTTTATTAATAATTTATCTGAACTACAC	5183
OY	61	AATATATPATACACTGTGCAGCGCAAGAACCTGCCAATCGCGCAATACCATAACAGA	120
DB	5182	AATATATPATACACTGTGCAGCGCAAGAACCTGCCAATACCATAACAGA	5123
OY	121	TCCACACCACTTAAATCATCATAAACAATCTGATTTGTAGTCGACAGACTATATTGAGTAGTG	180
DB	5122	TCCACACCACTTAAATCATCATAAACAATCTGATTTGTAGTCGACAGACTATATTGAGTAGTG	5063
OY	181	AACAACAATAGCACATTTAAGCATTTAGAGATTTATGGCTACTCTGCAATTCATATTTCT	240
DB	5062	AACAACAATAGCACATTTAAGCATTTAGAGATTTATGGCTACTCTGCAATTCATATTTCT	5003
OY	241	GATGCGCTGAATCTGTCGCATTTTACGCGTCCAGAAAGAAATTCACAAATCCTTGAGCAAT	300
DB	5002	GATGCGCTGAATCTGTCGCATTTTACGCGTCCAGAAAGAAATTCACAAATCCTTGAGCAAT	4943
OY	301	GTTGGCACTGSAAGCTGTTCGATGTTTTCATCTCTTAATTAACGTAGCAAGSAGTAGAT	360
DB	4942	GTTGGCACTGSAAGCTGTTCGATGTTTTCATCTCTTAATTAACGTAGCAAGSAGTAGAT	4883
OY	361	TATTTATGTACACAGAGAAATCTCTTAAGTCTTTTCCAACATGCAATGTCTGTAAAGAACAG	420
DB	4882	TATTTATGTACACAGAGAAATCTCTTAAGTCTTTTCCAACATGCAATGTCTGTAAAGAACAG	4823
OY	421	ATACAGTGAACCTTAAGTTTGTAAATGACAGCGTCAATGSCATTTTCTGGAAGGCATGTTCA	480
DB	4822	ATACAGTGAACCTTAAGTTTGTAAATGACAGCGTCAATGSCATTTTCTGGAAGGCATGTTCA	4763
OY	481	AGATGATGATTTCTGCGATCCTTGGAGGGGCCCTGAATTCGGAATACGTTAGTTGAGTT	540
DB	4762	AGATGATGATTTCTGCGATCCTTGGAGGGGCCCTGAATTCGGAATACGTTAGTTGAGTT	4703
OY	541	TTTGTATCCCAATAGCTTGGCTTAATTAACGTGAATTAAGCAATTTCTGTAAAGTGAAGTTTC	600
DB	4702	TTTGTATCCCAATAGCTTGGCTTAATTAACGTGAATTAAGCAATTTCTGTAAAGTGAAGTTTC	4643
OY	601	TACCATCTCACAGGAATAATTAAGCTAATACCTGTCCAAAGTGTGCGGCAATTTGACCAA	660
DB	4642	TACCATCTCACAGGAATAATTAAGCTAATACCTGTCCAAAGTGTGCGGCAATTTGACCAA	4583
OY	661	ATGAGATATCACAGCAATGCGAAGATGCAATCTGGCAAAAGAGCGGGAATTAATTTGTAT	720
DB	4582	ATGAGATATCACAGCAATGCGAAGATGCAATCTGGCAAAAGAGCGGGAATTAATTTGTAT	4523
OY	721	TCATCATATGGAACAGGAAACATATCATATGTTGCCACAGAGAGCCCGCGAGATTAAG	780

Dd	1172	TACATCTCCACAGGAAATAAAGGTAAATACCTGTCCAAAGAGTGTGGGCAATTTTGACAAA	122
Oy	661	ATGAGATATCAGACATATGGCAAGAAATGGCAATCTGGCAAAAGAGGGAAATATATGTAT	720
Dd	1232	ATGAGATATCAGACATATGGCAAGAAATGGCAATCTGGCAAAAGAGGGAAATATATGTAT	1291
Oy	721	TCTACTACATCGAAGAGAACATATACATATGTTGGCCGACAGAGAACCCCGGAGATAG	780
Dd	1292	TCTACTACATCGAAGAGAACATATATATGTTGGCCGACAGAGAACCCCGGAGATAG	1351
Oy	781	TTCCTGTCTTCCAGACAGAAATATCCGCACTGTATACGTCCCAACAATGAATATTCAAA	840
Dd	1352	TTCCTGTCTTCCAGACAGAAATATCCGCACTGTATACGTCCCAACAATGAATATTCAAA	1411
Oy	841	ACCACATCGGCTCAGAGAGAGCTTATGATATAAAGGCACTAATTTCTGATATTTTCTTACA	900
Dd	1412	ACCACATCGGCTCAGAGAGAGCTTATGATATAAAGGCACTAATTTCTGATATTTTCTTACA	1471
Oy	901	AAGCAATATATATATACACACCTTGAACCTTCACCAAGAGCTTGTGATTCGACTTGTGCC	960
Dd	1472	AAGCAATATATATATACACACCTTGAACCTTCACCAAGAGCTTGTGATTCGACTTGTGCC	1531
Oy	961	CATGAATATGCAATTCGACATTCGTGTCACTCTCAGAAATCTCGGAAATAAGAGAGGCA	1020
Dd	1532	CATGAATATGCAATTCGACATTCGTGTCACTCTCAGAAATCTCGGAAATAAGAGAGGCA	1591
Oy	1021	TAGCTTCCTGTGTGTGTGTGTGGATATATACGTGTCTAAACCTTGTGTGTGATCTG	1080
Dd	1592	TAGCTTCCTGTGTGTGTGTGTGGATATATACGTGTCTAAACCTTGTGTGTGATCTG	1651
Oy	1081	ATCTGTGTAGAGAGCACTGCTGTTATATACACTTATAAATATGTATATATATCTCTCAAG	1140
Dd	1652	ATCTGTGTAGAGAGCACTGCTGTTATATACACTTATAAATATGTATATATATCTCTCAAG	1711
Oy	1141	AACCTATATACGCAAGAAAGATATAGTGTGTGGATATGAGAGCCGTGAAAGGAGAC	1200
Dd	1712	AACCTATATACGCAAGAAAGATATAGTGTGTGGATATGAGAGCCGTGAAAGGAGAC	1771
Oy	1201	AAGCAATATACGTTACCTTACCAAGATGTGTTGCCAGACATATGGCAACCTCATTTCTACAC	1260
Dd	1772	AAGCAATATACGTTACCTTACCAAGATGTGTTGCCAGACATATGGCAACCTCATTTCTACAC	1831
Oy	1261	CAGAGAGCAAGAGCAAGTTTATGCTGTCAAAAAGATATGCTAGAGGCTTTCAGAAT	1320
Dd	1832	CAGAGAGCAAGAGCAAGTTTATGCTGTCAAAAAGATATGCTAGAGGCTTTCAGAAT	1891
Oy	1321	ATGTTCTATCTCAGACAGAACCAATGGGGCAAAATTTACTACTATTTGCCATCAATTAAC	1380
Dd	1892	ATGTTCTATCTCAGACAGAACCAATATGGGGCAAAATTTACTACTATTTGCCATCAATTAAC	1951
Oy	1381	CAGCTAAATAGCTCTACACTCAACCTAATGTTGAAACGGTCTGTCTGGCCACGGCTGAG	1440
Dd	1952	CAGCTAAATAGCTCTACACTCAACCTAATGTTGAAACGGTCTGTCTGGCCACGGCTGAG	2011
Oy	1441	AATGCACTTAATGAGAGGAGAACACTCTCTTTTCAACCTGCTACTGCTATCATCTGTAGAC	1500
Dd	2012	AATGCACTTAATGAGAGGAGAACACTCTCTTTTCAACCTGCTACTGCTATCATCTGTAGAC	2071
Oy	1501	GGTGAGAGCGGTGAGTCTTTCGCAATGACAGCTGCTTGTGTTGTCATCACTTGGCCAC	1560
Dd	2072	GGTGAGAGCGGTGAGTCTTTCGCAATGACAGCTGCTTGTGTTGTCATCACTTGGCCAC	2131
Oy	1561	GTTTGCACCGTGTACTACTCTCCCAATTGTCGCCCGGCTGTCCGGGCTGTAAAGAGCA	1620
Dd	2132	GTTTGCACCGTGTACTACTCTCCCAATTGTCGCCCGGCTGTCCGGGCTGTAAAGAGCA	2191
Oy	1621	CAGAGAGAGCGGCGCCACATATACCACTCTTACATCCCGTGTCCAGCAGAGAGATCCAT	1680
Dd	2192	CAGAGAGAGCGGCGCGAGATATACCACTCTTACATCCCGTGTCCAGCAGAGAGATCCAT	2251
Oy	1681	CAGGCGCTGGCGATG 1695	
Dd	2252	CAGGCGCTGGCGATG 2266	

[illegible]

OY 721 TCTACTACATGACAGAACCAATATCAATGTTGCCCGCAGAGACCCCGCAGATTAAG 780
|||||
Db 1292 TCTACTACATGACAGAACCAATATCAATGTTGCCCGCAGAGACCCCGCAGATTAAG 1351
OY 781 TTCCTGTTCTTCCACAGCAGAAATATCCGCAACTGCATATGCTCCACACATGAATTCGAAA 840
|||||
Db 1352 TTCCTGTTCTTCCACAGCAGAAATATCCGCAACTGCATATGCTCCACACATGAATTCGAAA 1411
OY 841 ACCACATGCGCTCAGAGAGAGTATGATTAAGGCACTAATTCGATTAATTTCTGAGA 900
|||||
Db 1412 ACCACATGCGCTCAGAGAGAGTATGATTAAGGCACTAATTCGATTAATTTCTGAGA 1471
OY 901 AAGCGAATAAATATATGACACACCTTGACCTCCACAGAGAGCTTGTGATCGACTTGTGCC 960
|||||
Db 1472 AAGCGAATAAATATATGACACACCTTGACCTCCACAGAGAGCTTGTGATCGACTTGTGCC 1531
OY 961 CATGAATATGCAATTCGTACATTTCTGCTACTGTCAGAATCTCTCGGAAAATGAGAGGCA 1020
|||||
Db 1532 CATGAATATGCAATTCGTACATTTCTGCTACTGTCAGAATCTCTCGGAAAATGAGAGGCA 1591
OY 1021 TAGCTTCGTGTTGATGATGTTGTTGGATATTACGCTGCTAAAACTTTGTTTCTGATCG 1080
|||||
Db 1592 TAGCTTCGTGTTGATGATGTTGTTGGATATTACGCTGCTAAAACTTTGTTTCTGATCG 1651
OY 1081 ATCTGTTAGAGAGCATGCTCTTTTAAAGCACTTAAAAATGTTAGTATATCTCTCAAGG 1140
|||||
Db 1652 ATCTGTTAGAGAGCATGCTCTTTTAAAGCACTTAAAAATGTTAGTATATCTCTCAAGG 1711
OY 1141 AGCCTATCTGCGCAAGAAAGATAGCTTGGCTGTGGGATTTGAGCCGTTGAAGGAAC 1200
|||||
Db 1712 AGCCTATCTGCGCAAGAAAGATAGCTTGGCTGTGGGATTTGAGCCGTTGAAGGAAC 1771
OY 1201 AAGCAATACATTTACCTTACCTACAGATGTTTGCACGACATGGGCAAGCTATTGCTAGAC 1260
|||||
Db 1772 AAGCAATACATTTACCTTACCTACAGATGTTTGCACGACATGGGCAAGCTATTGCTAGAC 1831
OY 1261 CAAGAAGGCAAGCAAGCAAAATTTAGCTGTCAAAAAAGATATGCTAGAGGCTTTCAGAAAT 1320
|||||
Db 1832 CAAGAAGGCAAGCAAGCAAAATTTAGCTGTCAAAAAAGATATGCTAGAGGCTTTCAGAAAT 1891
OY 1321 ATGTTTATCTACGCGACGACCAATGGGGCAAAATTTACTATTTGGCATACATTAAC 1380
|||||
Db 1892 ATGTTTATCTACGCGACGACCAATGGGGCAAAATTTACTATTTGGCATACATTAAC 1951
OY 1381 CACGTTAAAGTCTCTACACTCACTAACCTTAACTGTTGAAGGTCCTGTTCTGGCCAAGGTTGAG 1440
|||||
Db 1952 CACGTTAAAGTCTCTACACTCACTAACCTTAACTGTTGAAGGTCCTGTTCTGGCCAAGGTTGAG 2011
OY 1441 AATGCACCTAATGAGAGGAGCAACACTTCTTTCACCGTCTACTGCTACATCCTGTAGAC 1500
|||||
Db 2012 AATGCACCTAATGAGAGGAGCAACACTTCTTTCACCGTCTACTGCTACATCCTGTAGAC 2071
OY 1501 GGTGGACGGGTGAGGTGCTTTGGCCATGACCGTCCCTTGGTTGTGAGTCACTTGCGCAC 1560
|||||
Db 2072 GGTGGACGGGTGAGGTGCTTTGGCCATGACCGTCCCTTGGTTGTGAGTCACTTGCGCAC 2131
OY 1561 GGTGGACGGGTGACTACCTTGCCACATTTGCCCGCGCTGCGCGGCGCTTACAAAAAGCCA 1620
|||||
Db 2132 GGTGGACGGGTGACTACCTTGCCACATTTGCCCGCGCTGCGCGGCGCTTACAAAAAGCCA 2191
OY 1621 CACACGACGCGCGGCGCAGATTAACCATCTTACGATCCCGGTGTCAGCAAGAGATCCAT 1680
|||||
Db 2192 CACACGACGCGCGGCGCAGATTAACCATCTTACGATCCCGGTGTCAGCAAGAGATCCAT 2251
OY 1681 CAAGCGGTGCGCATG 1695
|||||
Db 2252 CAAGCGGTGCGCATG 2266

